Transcriptome analysis of temporal regulation of carbon metabolism by CcpA in Bacillus subtilis reveals additional target genes

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Published in:
Journal of Molecular Microbiology and Biotechnology

DOI:
10.1159/000096463

Supplementary material

Table S1
Differentially expressed genes in time. The data in this table has been simplified (see below) to increase readability. Genes with an expression ratio Δ*ccpA*/wt ≥ 2 at least in one of the investigated time points (values below 1 were converted by the formula [-1] × [1/ratio value]) and a Cyber-T (Bayes) *p*-value below 0.01, were selected for further analyses. For the selected genes, the expression ratio for the remaining time- points is shown if Δ*ccpA*/wt was at least 1.5 times with a *p* value below 0.05. The remaining expression ratios were set to 1. Different predictions of *cre* sites are included as well as the comparison to previous whole-transcriptome CcpA analyses [Yoshida et al., 2001; Moreno et al., 2001; Lorca et al., 2005; Blencke et al., 2006].

Table S2
Genes with assigned gene expression profiles resulting from STEM clustering. The maximum unit change was set to one (ratio change of 2 in $\log_2$ scale) in 15 model profiles between the time points.

Table S3
Comparison of the targets emerging from five transcriptome data sets [Yoshida et al., 2001; Moreno et al., 2001; Lorca et al., 2005; Blencke et al., 2006]. A group of 52 genes are differentially expressed in at least three out of five datasets. These genes likely belong to the CcpA-regulon and they are not listed yet in the DBTBS database.

Table S4
The uniquely differentially expressed genes in this study compared to other whole-transcriptome studies [Yoshida et al., 2001; Moreno et al., 2001; Lorca et al., 2005; Blencke et al., 2006].

Table S5
Genes showing altered expression patterns in the stationary phase.

Fig. S1
Weight matrix based on the known *cre* elements from the DBTBS database. This matrix was used to search the genome sequence of *B. subtilis* for putative *cre* transcription factor binding sites.